AMENDMENT TO THE SPECIFICATION

Please amend paragraph [0012] of the application as published (US 20070264715) as follows:

[**0012**] Homologues of LuxR are proteins that share a common evolutionary ancestor with LuxR (as described by Gray & Garey, 2001, Microbiology, 147:2379-2387) and are induced in quorum sensing. Homologues of LuxR are described in PROSITE as being members of the LuxR family of proteins ~~(see http://us.expasy.org/cgi-bin/nicedoc.pl?PS00622)~~. Preferably they are proteins that are found on the outer surface of bacterial membranes during the pre-quorate and quorate phases of bacterial growth and which bind a signaling molecule and are then able to activate transcription. Preferably, they are proteins that share sequence identity with LuxR. Preferably homologues of LuxR share more than 40% sequence identity with LuxR (e.g. more than 50%, 60%, 70%, 80%, 90%, 95%, 99% or more). Preferably homologues of LuxR have residues corresponding to those of LuxR. Preferably homologues of LuxR have residues corresponding to the following residues of LuxR when aligned using the Clustal alignment algorithm: TRP66, TYR70, ASP79, PRO80, GLY121, GLU187 and GLY197. Preferably the homologue of LuxR is selected from the group consisting of AhlR, AhyR, AsaR, BafR, Bis R, BpsR, BviR, CarR, CepR, CerR, CinR, CsaR, CviR, EagR, EcbR, EchR, EsaR, ExpR, HalR, LasR, LuxS, M18752, MupR, PcoR, PhzR, PmlR, PpuR, PsmR, PsyR, RaiR, RhiR, RhlR, SdiA, SdiR, SmaR, SolR, SpnR, SprR, SwrR, TraR, TriR, TrIR, TrnR, VanR, VsmR, Y4qH, YenR, YpeR, YpsR, YruR, YtbR and YukR.

Please amend paragraph [0023] of the application as published (US 20070264715) as follows:

[**0023**] Treatment of bacteria with a peptide hydrolase inhibitor may be used to upregulate quorum sensing in any species of bacteria that utilises this system. Preferably quorum sensing is upregulated in bacteria selected from the list consisting of *Bacillus subtilis, Streptococcus pneumoniae, Staphylococcus aureas, Vibrio salmonicida, Aeromonas hydrophila, ~~Burkhoderia~~Burkholderia ambifaria, Burkholderia pseudomallei, Burkholderia*

mallei, Burkholderia stabilis, Burkholderia vietnamiensis, Burkholderia multivorans, Escherichia coli, Serratia marcescens, Salmonella typhi, Brucella suis, Brucella melitensis, Yersinia ruckeri, Hafina alvei, Shigella flexneri, Serratia liquefaciens, Enterococcus faecalis, Pseudomonas aeruginosa, Burkholderia cepacia, Pseudomonas fluorescens, Providencia stuartii, Klebsiella aerogenes, Yersinia pestis, Yersinia enterocolitica or *Yersinia pseudotuberculosis*.

Please amend paragraph [0027] of the application as published (US 20070264715) as follows:

[**0027**] Peptide hydrolases are enzymes or compounds that irreversibly hydrolyse amide bonds in peptides and proteins. Peptide hydrolases are widely distributed and are involved in many different biological processes, from activation of proteins and peptides to degradation of proteins.

Please amend paragraph [0031] of the application as published (US 20070264715) as follows:

[**0031**] The Peptide Cutter tool ~~(see http://us.expasy.org/tools/peptidecutter/peptidecutter_instructions.html)~~ may be used to decide which particular peptide hydrolase should be use for a particular homologue of LuxR.